

Shashank
Paper #5



ENTERED PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,048

DATE: 04/10/2002

TIME: 13:09:08

Input Set : A:\019048.dos

Output Set: N:\CRF3\04102002\J019048.raw

4 <110> APPLICANT: Heinz, Ernst
 5 Girke, Thomas
 6 Scheffler, Jodi
 7 Da Costa e Silva, Oswaldo
 9 <120> TITLE OF INVENTION: Plants expressing 6-desaturase genes, PUFAS-containg oils
 from these
 10 plants, and a process for the preparation of unsaturated fatty acids
 12 <130> FILE REFERENCE: 0093/000032
 W--> 13 <140> CURRENT APPLICATION NUMBER: US 10/019,048
 C--> 14 <141> CURRENT FILING DATE: 2002-03-19
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP00/006223
 17 <151> PRIOR FILING DATE: 2000-07-04
 19 <160> NUMBER OF SEQ ID NOS: 2
 21 <170> SOFTWARE: WordPerfect version 6.1
 25 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2012
 29 <212> TYPE: DNA
 31 <213> ORGANISM: Physcomitrella patens
 35 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 39 <222> LOCATION: (319)..(1896)
 43 <400> SEQUENCE: 1
 45 ccgagtcgcg gatcagccat cgcccccca gggccgcctg catttgttgg gacggtgttg 60
 47 gaggaggagg cagatgcgcg ggcgttggtg gagtcgtcat ccgaggatct actgcggcaa 120
 49 tacctccggg ttttggagcg ggcaaactct gttgcggctc ggaaggctat aggttcggca 180
 51 ggagactgtt gatTTtatgt cggggcatt gccattgtgg agagcggggg agactcagga 240
 53 tctgtgatgt tgctgtgcgc gccccactg ccgcagacgc tctgtgtatg acgagggtgt 300
 55 tgtggagcgg ctTTTgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351
 56 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly
 57 1 5 10
 59 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc 399
 60 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu
 61 15 20 25
 63 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc 447
 64 Phe Ser Asp Phe Phe Tyr Val Ser Ser Thr Val Gly Ser Trp Ser
 65 30 35 40
 67 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt 495
 68 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val
 69 45 50 55
 71 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat 543
 72 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn
 73 60 65 70 75
 75 tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag 591
 76 Ser Ser Thr Gln Glv Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys

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77	80	85	90	
79	ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta			639
80	Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu			
81	95	100	105	
83	tca gaa gta gca gta cac aac aag cca agc gat tgc tgg att gtt gta			687
84	Ser Glu Val Ala Val His Asn Lys Pro Ser Asp Cys Trp Ile Val Val			
85	110	115	120	
87	aaa aac aag gtg tat gat gtt tcc aat ttt gcg gac gag cat ccc gga			735
88	Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly			
89	125	130	135	
91	gga tca gtt att agt act tat ttt gga cga gac ggc aca gat gtt ttc			783
92	Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe			
93	140	145	150	155
95	tct agt ttt cat gca gct tct aca tgg aaa att ctt caa gac ttt tac			831
96	Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr			
97	160	165	170	
99	att ggt gac gtg gag agg gtg gag ccg act cca gag ctg ctg aaa gat			879
100	Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp			
101	175	180	185	
103	ttc cga gaa atg aga gct ctt ttc ctg agg gag caa ctt ttc aaa agt			927
104	Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser			
105	190	195	200	
107	tcg aaa ttg tac tat gtt atg aag ctg ctc acg aat gtt gct att ttt			975
108	Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe			
109	205	210	215	
111	gct gcg agc att gca ata ata tgt tgg agc aag act att tca gcg gtt			1023
112	Ala Ala Ser Ile Ala Ile Cys Trp Ser Lys Thr Ile Ser Ala Val			
113	220	225	230	235
115	ttg gct tca gct tgt atg atg gct ctg tgt ttc caa cag tgc gga tgg			1071
116	Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp			
117	240	245	250	
119	cta tcc cat gat ttt ctc cac aat cag gtg ttt gag aca cgc tgg ctt			1119
120	Leu Ser His Asp Phe Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu			
121	255	260	265	
123	aat gaa gtt gtc ggg tat gtg atc ggc aac gcc gtt ctg ggg ttt agt			1167
124	Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser			
125	270	275	280	
127	aca ggg tgg tgg aag gag aag cat aac ctt cat cat gct gct cca aat			1215
128	Thr Gly Trp Trp Lys Glu Lys His Asn Leu His His Ala Ala Pro Asn			
129	285	290	295	
131	gaa tgc gat cag act tac caa cca att gat gaa gat att gat act ctc			1263
132	Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu			
133	300	305	310	315
135	ccc ctc att gcc tgg agc aag gac ata ctg gcc aca gtt gag aat aag			1311
136	Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys			
137	320	325	330	
139	aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg			1359
140	Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu			
141	335	340	345	

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143 tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg agc tgg aga tat acc	1407
144 Leu Phe Ala Arg Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr	
145 350 355 360	
147 tct aca gca gtg ctc tca cct gtc gac agg ttg ttg gag aag gga act	1455
148 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr	
149 365 370 375	
151 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc	1503
152 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu	
153 380 385 390 395	
155 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc	1551
156 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser	
157 400 405 410	
159 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag	1599
160 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu	
161 415 420 425	
163 gtt tat aat tcg tct aaa gaa ttc gtg agt gca cag atc gta tcc aca	1647
164 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr	
165 430 435 440	
167 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt	1695
168 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu	
169 445 450 455	
171 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat	1743
172 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn	
173 460 465 470 475	
175 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt	1791
176 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly	
177 480 485 490	
179 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg	1839
180 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu	
181 495 500 505	
183 aaa gca ttg aag gaa gtc gcg gag gct gca gag cag cat gct acc	1887
184 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Glu Gln His Ala Thr	
185 510 515 520	
187 acc agt taa cagtcttgg aaagcttggc aattgatctt tattctccac	1936
188 Thr Ser	
189 525	
191 ggcagttgt tggtttttt ggggtgaatg accgaatgta ctggcatcca ttcttctgta	1996
193 gccatcaatt ttgaac	2012
197 <210> SEQ ID NO: 2	
199 <211> LENGTH: 525	
201 <212> TYPE: PRT	
203 <213> ORGANISM: Physcomitrella patens	
205 <400> SEQUENCE: 2	
207 Met Val Phe Ala Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn	
208 1 5 10 15	
210 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe	
211 20 25 30	
213 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln	
214 35 40 45	

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216 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
217      50          55          60
219 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
220   65          70          75          80
222 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
223           85          90          95
225 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
226           100         105         110
228 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
229           115         120         125
231 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
232           130         135         140
234 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
235   145         150         155         160
237 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
238           165         170         175
240 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
241           180         185         190
243 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
244           195         200         205
246 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
247   210         215         220
249 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
250   225         230         235         240
252 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
253           245         250         255
255 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
256           260         265         270
258 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
259           275         280         285
261 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
262   290         295         300
264 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
265   305         310         315         320
267 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
268           325         330         335
270 Leu Gln Tyr Gln His Leu Phe Met Gly Leu Leu Phe Phe Ala Arg
271           340         345         350
273 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
274           355         360         365
276 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
277           370         375         380
279 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
280   385         390         395         400
282 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
283           405         410         415
285 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
286           420         425         430
288 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly

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289	435	440	445
291	Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu		
292	450	455	460
294	His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala		
295	465	470	475
297	Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp		480
298	485	490	495
300	Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu		
301	500	505	510
303	Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser		
304	515	520	525

VERIFICATION SUMMARY
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Input Set : A:\019048.dos
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L:13 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date